

SEQUENCE LISTING

<110> Neff, Michael M.
Chory, Joanne

<120> GENETICALLY MODIFIED PLANTS HAVING
MODULATED BRASSINOSTEROID SIGNALING

<130> SALKINS.024DV1

<150> US 09/527,073

<151> 2000-03-16

<150> US 60/124570

<151> 1999-03-16

<150> US 60/170,931

<151> 1999-12-14

<150> US 60/172,832

<151> 1999-12-20

<160> 16

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 1563

<212> DNA

<213> Arabidopsis thaliana

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<223> Oligonucleotide

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catttctcta aacaaggaat tcgaggtcct ccttatcatt tcttcatcgg aaatgttaaa 180
gaacttggtg gaatgatgct taaagcttct tctcatccta tgcctttctc tcacaatatt 240
cttcctagag ttctctcttt ttaccatcac tggagaaaaa tctacggtgc tacatttctg 300
gtttggttcg gtccaacttt cgggttaacg gtagccgac ctgatttgat cagagagatc 360
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ggcgatggac tacttagtct caaagggtgaa aaatgggctc atcatcgaaa aatcattagc 480
cctacttttc atatggagaa tcttaagttg cttgtaccag ttgtgttgaa gagtgtgact 540
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tatgaagatg gtcgagcagt ttttcgactt caagctcaac aaatgcttct ttgtgctgaa 720
gcttttcaaa aagcttctcat tcctggctat agattttttc cgacaagagg gaatttgaa 780
tctcggaagt tagacaagga gataaggaag tcgttggtga agctgataga gcggcggaga 840
caaacgcta tagatggaga aggggaagaa tgtaaggagc cggcggcgaa ggatttggtg 900
ggattaatga ttcaggcaaa gaatgtgacg gttcaggaca ttgtggagga gtgtaaaagc 960
tttttcttcg ccgggaaaca gacaacttct aatctgctga cgtggacgac catcttgcta 1020
tccatgcacc cggagtggca ggccaaagca cgtgatgagg tcctcagggc ctgcgggtca 1080
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Figure 1 displays 12 histograms, labeled x_0 through x_{11} , showing the distribution of the number of non-zero elements in the vector x_k for $k = 0, 1, \dots, 11$. The x-axis for each histogram represents the number of non-zero elements (0 to 10), and the y-axis represents the count (0 to 10). The distributions are roughly bell-shaped and centered around 5, with the peak count increasing from 10 at $k=0$ to 12 at $k=11$.

<400>	2															
Met	Glu	Glu	Glu	Ser	Ser	Ser	Trp	Phe	Ile	Pro	Lys	Val	Leu	Val	Leu	
1				5					10					15		
Ser	Val	Ile	Leu	Ser	Leu	Val	Ile	Val	Lys	Gly	Met	Ser	Leu	Leu	Trp	
			20					25					30			
Trp	Arg	Pro	Arg	Lys	Ile	Glu	Glu	His	Phe	Ser	Lys	Gln	Gly	Ile	Arg	
		35				40						45				
Gly	Pro	Pro	Tyr	His	Phe	Phe	Ile	Gly	Asn	Val	Lys	Glu	Leu	Val	Gly	
	50					55					60					
Met	Met	Leu	Lys	Ala	Ser	Ser	His	Pro	Met	Pro	Phe	Ser	His	Asn	Ile	
65				70						75				80		
Leu	Pro	Arg	Val	Leu	Ser	Phe	Tyr	His	His	Trp	Arg	Lys	Ile	Tyr	Gly	
			85						90					95		
Ala	Thr	Phe	Leu	Val	Trp	Phe	Gly	Pro	Thr	Phe	Arg	Leu	Thr	Val	Ala	
			100					105					110			
Asp	Pro	Asp	Leu	Ile	Arg	Glu	Ile	Phe	Ser	Lys	Ser	Glu	Phe	Tyr	Glu	
		115					120					125				
Lys	Asn	Glu	Ala	His	Pro	Leu	Val	Lys	Gln	Leu	Glu	Gly	Asp	Gly	Leu	
	130					135					140					
Leu	Ser	Leu	Lys	Gly	Glu	Lys	Trp	Ala	His	His	Arg	Lys	Ile	Ile	Ser	
145					150					155					160	
Pro	Thr	Phe	His	Met	Glu	Asn	Leu	Lys	Leu	Leu	Val	Pro	Val	Val	Leu	
			165						170					175		
Lys	Ser	Val	Thr	Asp	Met	Val	Asp	Lys	Trp	Ser	Asp	Lys	Leu	Ser	Glu	
		180						185					190			
Asn	Gly	Glu	Val	Glu	Val	Asp	Val	Tyr	Glu	Trp	Phe	Gln	Ile	Leu	Thr	
		195					200					205				
Glu	Asp	Val	Ile	Ser	Arg	Thr	Ala	Phe	Gly	Ser	Ser	Tyr	Glu	Asp	Gly	
	210					215					220					
Arg	Ala	Val	Phe	Arg	Leu	Gln	Ala	Gln	Gln	Met	Leu	Leu	Cys	Ala	Glu	
225					230					235				240		
Ala	Phe	Gln	Lys	Val	Phe	Ile	Pro	Gly	Tyr	Arg	Phe	Phe	Pro	Thr	Arg	
			245						250					255		
Gly	Asn	Leu	Lys	Ser	Arg	Lys	Leu	Asp	Lys	Glu	Ile	Arg	Lys	Ser	Leu	
		260						265					270			
Leu	Lys	Leu	Ile	Glu	Arg	Arg	Arg	Gln	Asn	Ala	Ile	Asp	Gly	Glu	Gly	
		275					280					285				
Glu	Glu	Cys	Lys	Glu	Pro	Ala	Ala	Lys	Asp	Leu	Leu	Gly	Leu	Met	Ile	
	290					295					300					
Gln	Ala	Lys	Asn	Val	Thr	Val	Gln	Asp	Ile	Val	Glu	Glu	Cys	Lys	Ser	

305		310		315		320
Phe Phe Phe Ala Gly Lys Gln Thr Thr Ser Asn Leu Leu Thr Trp Thr						
	325			330		335
Thr Ile Leu Leu Ser Met His Pro Glu Trp Gln Ala Lys Ala Arg Asp						
	340			345		350
Glu Val Leu Arg Val Cys Gly Ser Arg Asp Val Pro Thr Lys Asp His						
	355			360		365
Val Val Lys Leu Lys Thr Leu Ser Met Ile Leu Asn Glu Ser Leu Arg						
	370			375		380
Leu Tyr Pro Pro Ile Val Ala Thr Ile Arg Arg Ala Lys Ser Asp Val						
	385			390		395
Lys Leu Gly Gly Tyr Lys Ile Pro Cys Gly Thr Glu Leu Leu Ile Pro						
	405			410		415
Ile Ile Ala Val His His Asp Gln Ala Ile Trp Gly Asn Asp Val Asn						
	420			425		430
Glu Phe Asn Pro Ala Arg Phe Ala Asp Gly Val Pro Arg Ala Ala Lys						
	435			440		445
His Pro Val Gly Phe Ile Pro Phe Gly Leu Gly Val Arg Thr Cys Ile						
	450			455		460
Gly Gln Asn Leu Ala Ile Leu Gln Ala Lys Leu Thr Leu Ala Val Met						
	465			470		475
Ile Gln Arg Phe Thr Phe His Leu Ala Pro Thr Tyr Gln His Ala Pro						
	485			490		495
Thr Val Leu Met Leu Leu Tyr Pro Gln His Gly Ala Pro Ile Thr Phe						
	500			505		510
Arg Arg Leu Thr Asn His Glu Asp						
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<223> Primer

<400> 3

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<211> 20

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 <210> 7
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<210> 11
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<210> 12
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<210> 14
<211> 31
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<210> 15
<211> 32
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32

<210> 16
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atctctttct tgatctctct ctataaaagc tcaaatagcc cagcaagcaa aataatccaa 180
aaagaaacca agataagaag aaacaaactc gcaaagaaac aaaaaggaaa aaaaaaaaaa 240
aaacgaatta aaaaaagaag aaataaatcc tcctttttaa caccctcatt cctctttctc 300
cggcactcaa aagagaccaa agaagaaaac tttagctctc ctttttgtgt tttctctctt 360
ttctttgttg gtgttccgac aatggaggaa gaaagtagca gctggttcat tccaaagggt 420
cttgttctgt ctgtaatctt aagtccttgt aatagtgaag ggtatgtctc tgttatgggt 480
gagaccaaga aagattgaag aacatttctc taaacaagga attcgaggtc ctccttatca 540
tttcttcctc ggaaatgtta aagaacttgt tgaatgatgc tttaaagct 588